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Title: Building a canonical model of the human mitotic cell

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Abstract— The execution of mitosis requires that the activity of protein complexes be tightly coordinated in space and time but our knowledge of the dynamics and interactions of the several hundred proteins required for mitosis is incomplete and fragmented due to lack of systematic and quantitative approaches. In addition, the few existing models only offer limited insight into oversimplified and isolated aspects of mitosis. To tackle this situation, our group uses automated fluorescence imaging of live dividing cells, image analysis and machine learning approaches to build a canonical model of a human dividing cell that can be used to integrate data from different experiments. The simultaneous visualization of multiple proteins in the model cell can be used to generate new testable hypotheses about protein functions in mitosis.

Index Terms—Mitosis, model, confocal microscopy, live cell imaging, fluorescence correlation spectroscopy, segmentation, image registration, time series alignment, machine learning.

Bio: Jean-Karim Hériché was trained as an engineer and obtained a PhD in biology from Université Joseph Fourier in Grenoble, France for work carried out at the French Atomic Energy Commission. He did post-doctoral research on cell cycle control during Drosophila development in Patrick O'Farrell's lab at UCSF and then moved to Richard Durbin's group at the Wellcome Trust Sanger Institute where he implemented bioinformatics tools and analysis methods for the MitoCheck project. He is now in Jan Ellenberg's group at EMBL where he works on image-based systems